

<!--StartFragment-->RESULT 2

US-10-332-426-6

SEQ ID NO: 9 alignment

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; Sequence 6, Application US/10332426
; Publication No. US20040029136A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. Tom;
; APPLICANT: AZIMZAI, Yalda; DAS, Debopriya;
; APPLICANT: THORNTON, Michael; LU, Dyung Aina M.;
; APPLICANT: TRIBOULEY, Catherine M.; YUE, Henry;
; APPLICANT: GANDHI, Ameena R.; CHAWLA, Narinder K.;
; APPLICANT: KHAN, Farrah A.; LU, Yan;
; APPLICANT: YAO, Monique G.; HAFALIA, April J. A.;
; APPLICANT: ELLIOTT, Vicki S.; ARVIZU, Chandra S.;
; APPLICANT: LAL, Preeti; RAMKUMAR, Jayalaxmi;
; APPLICANT: NGUYEN, Danniel B.; BAUGHN, Mariah R.
; TITLE OF INVENTION: LIPID METABOLISM MOLECULES
; FILE REFERENCE: PI-0152 USN
; CURRENT APPLICATION NUMBER: US/10/332,426
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US 60/216,803
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/216,801
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/218,233
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/220,046
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/220,739
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/222,824
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 1026
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040029136A1 7477093CD1
US-10-332-426-6
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Query Match 98.0%; Score 4191; DB 4; Length 1026;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 803; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db      223 RGEASTCWLTVRVLEARNLRWADLLSEADPYVILQLSTAPGMKFKTKTLTDTSHPVWNE 282

Qy      75 AFRFLIQSQVKNVLELSIYDEDSVTEDDICFKVLYDISEVLP GKLLRKTFSQSPQGEEEL 134
      |||
Db      283 AFRFLIQSQVKNVLELSIYDEDSVTEDDICFKVLYDISEVLP GKLLRKTFSQSPQGEEEL 342

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Db      343 DVEFLMEETSDRPENLITNKVIVARELSCLDVHLDSTGSTAVVADQDKLELELVLKGSYE 402

Qy      195 DTQTSFLGTASAFRFHYMAALETELSGRLRSSRSNGWNGDNSAGYLTVPLRPLTIGKEVT 254
      |||
Db      403 DTQTSFLGTASAFRFHYMAALETELSGRLRSSRSNGWNGDNSAGYLTVPLRPLTIGKEVT 462
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Qy	255	MDVPAPNAPGVRLQLKAEGCPEELAVHLGFNLCAEEQAFLSRRKQVVAKALKQALQLDRD	314
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Qy	315	LQEDEVPPVVGIMATGGGARAMTSLYGHLLALQKLGLLDCVTYFSGISGSTWTMAHLYGDP	374
Db	523	LQEDEVPPVVGIMATGGGARAMTSLYGHLLALQKLGLLDCVTYFSGISGSTWTMAHLYGDP	582
Qy	375	EWSQRDLEGPIRYAREHLAKSKLEVFSPERLASRRELELRAEQGHPTTFVDLWALVLES	434
Db	583	EWSQRDLEGPIRYAREHLAKSKLEVFSPERLASRRELELRAEQGHPTTFVDLWALVLES	642
Qy	435	MLHGQVMDQKLSGQRAALERGQNPLPLYLSLNVKENNLETLDKFKEWVEFSPYEVGFLKYG	494
Db	643	MLHGQVMDQKLSGQRAALERGQNPLPLYLSLNVKENNLETLDKFKEWVEFSPYEVGFLKYG	702
Qy	495	AFVPPELFGSEFFMGRLMRRRIPEPRICFLEAIWSNIFSLNLLDAWYDLTSSGESWKQHIK	554
Db	703	AFVPPELFGSEFFMGRLMRRRIPEPRICFLEAIWSNIFSLNLLDAWYDLTSSGESWKQHIK	762
Qy	555	DKTRSLEKEPLTTSGTSSRLEASWLQPGTALAQAQFKGFLTGRPLHQSPNFLQGLQLHQD	614
Db	763	DKTRSLEKEPLTTSGTSSRLEASWLQPGTALAQAQFKGFLTGRPLHQSPNFLQGLQLHQD	822
Qy	615	YCSHKDFSTWADYQLDSMPSQLTPKEPRLCLVDAAYFINTSSPSMFRPGRRLDLILSFDY	674
Db	823	YCSHKDFSTWADYQLDSMPSQLTPKEPRLCLVDAAYFINTSSPSMFRPGRRLDLILSFDY	882
Qy	675	SLSAPFEALQQTELYCRARGLPFPRVEPSPQDQHQPCHLFSDPACPEAPILLHFPLVN	734
Db	883	SLSAPFEALQQTELYCRARGLPFPRVEPSPQDQHQPCHLFSDPACPEAPILLHFPLVN	942
Qy	735	ASFKDHSAPGVQRSPAELQGGQVDLTGATCPYTLSNMITYKEEDFERLLRLSDYNVQTSQG	794
Db	943	ASFKDHSAPGVQRSPAELQGGQVDLTGATCPYTLSNMITYKEEDFERLLRLSDYNVQTSQG	1002
Qy	795	AILQALRTALKHRTLEARPPRAQT	818
Db	1003	AILQALRTALKHRTLEARPPRAQT	1026

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